



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/925,055
Source: OIPÉ
Date Processed by STIC: 03/16/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/925,055

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
(OLD RULES)
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES)
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220> Sequence(s) 32 missing the <220> "Feature" and associated numeric identifiers and responses
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk

AMC - Biotechnology Systems Branch - 06/04/2001

may
The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/925,055

DATE: 08/16/2001

TIME: 13:28:58

Input Set : A:\00-56.txt

Output Set: N:\CRF3\08162001\I925055.raw

Doc: 00-56-0000

Form: 00-56-0000

4 <110> APPLICANT: Kindsvogel, Wayne R.

5 Popouzis, Stavros

6 <120> TITLE OF INVENTION: SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS

7 <130> FILE REFERENCE: 00-56

C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/925,055

C--> 11 <141> CURRENT FILING DATE: 2001-08-08

11 <150> PRIOR APPLICATION NUMBER: US 60/223,827

12 <151> PRIOR FILING DATE: 2000-08-08

14 <150> PRIOR APPLICATION NUMBER: US 60/250,876

15 <151> PRIOR FILING DATE: 2000-12-01

17 <160> NUMBER OF SEQ ID NOS: 31

19 <170> SOFTWARE: FastSEQ for Windows Version 3.0

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 2831

23 <212> TYPE: DNA

24 <213> ORGANISM: Homo sapien

26 <220> FEATURE:

27 <221> NAME/KEY: CDS

28 <222> LOCATION: (34)...(1755)

30 <400> SEQUENCE: 1

31 tagaggtccaa gggagggtctc tgtgccagac ccg atg agg acg ctg ctg acc atc 54

Met Arg Thr Leu Leu Thr Ile

1 5

35 ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tgg gat 102

36 Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp

37 10 15 20

39 ctg ctc cag cac gtg aca ttc cag tcc agc aag ttt gaa aac atc ctg 150

40 Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu

41 15 30 35

43 aag tgg gag agc ggg cca gag gcc acc cca gac acg gtc tac agc atc 198

44 Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile

45 40 45 50 55

47 gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag gga tgt 246

48 Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys

49 60 65 70

51 cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac 294

52 Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn

53 75 80 85

55 ctg acg gag ctg tac tat gcc agg gtc acc gct gtc agt ggc gga agc 342

56 Leu Thr Ser Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly

57 90 95 100

59 cag tca gtc acc aag atg act gac agc ttc aac tct ctg cag cac act 390

60 Arg Ser Ala Thr Lys Met Thr Asp Arg Ile Ser Ser Leu Gln His Thr

61 105 110 115

63 acc ctg aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tgg att 438

64 Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile

65 120 125 130 135

Entered
check diskette
8/16/01

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/925,055

DATE: 08-16-2001

TIME: 14:14:17

Input Set : A:\00-56.txt

Output Set: N:\CRF3\08162001\I925055.raw

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67  cag atg att gtt cat cat acc acc acc acc atc tyr gaa ggc gat gac 486
68  Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly
69          140          141          150
71  cag cgg cta acc ctg gaa gac atc ttc cat gac cta ttc tac cat tta 534
72  His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu
73          155          160          165
75  gag ctc cag gtc aac cgc acc tac caa atg sac ctt gga ggg aag cag 582
76  Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln
77          170          175          180
79  aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc 630
80  Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly
81          185          190          195
83  acc atc atg att tgc gtt ccc acc tgg gac aag gag agt gcc ccc tac 678
84  Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr
85          200          205          210          215
87  atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc 726
88  Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe
89          220          225          230
91  tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc 774
92  Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys
93          235          240          245
95  tac ctg agc tac aga tat gtc acc aag cag cct gca cct ccc aac tcc 822
96  Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser
97          250          255          260
99  ctg aac gtc cag cga gtc ctg act ttc cag cgg ctg cgc ttc atc cag 870
100  Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln
101          265          270          275
103  gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg 918
104  Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu
105          280          285          290          295
107  gcc cag cct gtc cag tac tcc cag atc agg gtg tat gga ccc agg gag 966
108  Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu
109          300          305          310
111  ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta 1014
112  Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu
113          315          320          325
115  ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc 1062
116  Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro
117          330          335          340
119  cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc 1110
120  Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val
121          345          350          355
123  gga ccc cca tac tat gaa cct cag gag acc acc aac gct aca ttc cat 1158
124  Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Trp Glu Ala Gln Phe Pro
125          360          365          370          375
127  ttc tac gcc cca cag gcc atc tat aag gtc aac cct tcc tcc tat acc 1206
128  Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala
129          380          385          390
131  cct caa gcc atc cag gcc agc tgg cct acc tac tat ggg gta tgc atg 1254

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/925,055

DATE: 08-16-2001

TIME: 12:22:58

Input Set : A:\00-56.txt

Output Set : N:\CRF3\08162001\I925055.raw

133	Pro	Gln	Ala	Thr	Pro	Asp	Ser	Tyr	Pro	Leu	Ser	Tyr	Gly	Val	Cys	Met	
134					395				400					405			
135	gaa	ggt	tct	ggc	aaa	gac	tcg	acc	agg	aca	ctt	tct	agt	ccg	aaa		1302
136	Glu	Gly	Ser	Gly	Lys	Asp	Ser	Pro	Thr	Gly	Thr	Leu	Ser	Ser	Pro	Lys	
137					410				415					420			
138	cac	ctt	agg	ccg	aaa	ggt	cag	ctt	cag	aaa	gag	cca	cca	gct	gga	agg	1350
139	His	Leu	Arg	Pro	Lys	Gly	Gln	Leu	Gln	Lys	Glu	Pro	Pro	Ala	Gly	Ser	
140					425				430					435			
141	tgc	atg	tta	ggt	ggc	ctt	tct	ctg	cag	gag	gtg	acc	tcc	ttg	gct	atg	1398
142	Cys	Met	Leu	Gly	Gly	Leu	Ser	Leu	Gln	Glu	Val	Thr	Ser	Leu	Ala	Met	
143					440				445					450			
144	gag	gaa	ttc	caa	gaa	gca	aaa	tca	ttg	cac	cag	acc	ctg	ggg	att	tgc	1446
145	Glu	Glu	Ser	Gln	Glu	Ala	Lys	Ser	Leu	His	Gln	Pro	Leu	Gly	Ile	Cys	
146					460				465					470			
147	aca	gac	aga	aca	tct	gac	cca	aat	gtg	cta	cac	agt	ggg	gag	gaa	ggg	1494
148	Thr	Asp	Arg	Thr	Ser	Asp	Pro	Asn	Val	Leu	His	Ser	Gly	Glu	Glu	Gly	
149					475				480					485			
150	aca	cca	cag	tac	cta	aag	ggc	cag	ctc	cca	ctc	ctc	tcc	tca	gtc	cag	1542
151	Thr	Pro	Gln	Tyr	Leu	Lys	Gly	Gln	Leu	Pro	Leu	Leu	Ser	Ser	Val	Gln	
152					490				495					500			
153	atc	gag	ggc	cca	ccc	atg	tcc	ctc	ccg	ttg	caa	ccg	ccg	tcc	ggg	cca	1590
154	Ile	Glu	Gly	His	Pro	Met	Ser	Leu	Pro	Leu	Gln	Pro	Pro	Ser	Gly	Pro	
155					505				510					515			
156	tgt	tcc	ccc	tcc	gac	caa	ggg	cca	agt	ccc	tgg	ggc	ctg	ctg	gag	tcc	1638
157	Cys	Ser	Pro	Ser	Asp	Gln	Gly	Pro	Ser	Pro	Trp	Gly	Leu	Leu	Glu	Ser	
158					520				525					530			
159	ctt	gtg	tgt	ccc	aag	gat	gaa	gcc	aag	agg	cca	gcc	ccg	gag	acc	tca	1686
160	Leu	Val	Cys	Pro	Lys	Asp	Glu	Ala	Lys	Ser	Pro	Ala	Pro	Glu	Thr	Ser	
161					540				545					550			
162	gac	ctg	gag	cag	ccc	aca	gaa	ctg	gat	tct	ctt	ttc	aga	ggg	ctg	gac	1734
163	Asp	Leu	Glu	Gln	Pro	Thr	Glu	Leu	Asp	Ser	Leu	Phe	Arg	Gly	Leu	Ala	
164					555				560					565			
165	ctg	act	gtg	cag	tgg	gag	tcc	tgagggggaat	gggaaaaggt	tggtgcttcc							1785
166	Leu	Thr	Val	Gln	Trp	Glu	Ser										
167					570												
168	tcctctgtcc	taccacgtgt	cacatccttg	gtgtgtcaatc	ccatgcctgc	ccatgcacaa											1845
169	cactcttgga	tctggctca	gacgggtgac	cttcagagaa	gcagagggag	tggtatgcag											1905
170	ggccctctgc	atgggtgggc	tcttcacggg	aacaaacag	catgataagg	actgcagggg											1965
171	gggagctctg	gggagcagct	tggttagaca	agccttctct	cgctgagccc	tgcacggcag											2025
172	aaatgacagt	gaaaggagga	aatgcaggga	aactctcgag	gtccagagcc	ccactctcta											2085
173	acaccatgga	ttcaaaatgc	tcagggaatt	tgcctctctt	tgcaccattc	ctggccagtt											2145
174	tcacaatcta	gtctgacaga	gcattgagcc	cttctctctt	ctgtcattgt	tcaaaatagg											2205
175	gaagagagcc	tggaaaagaa	ccaggcttgg	aaaacacaa	taaggaggct	ggaaacaa											2265
176	agaacaacct	gacttctgc	caaggccagg	gcaagagga	cgccaggact	ctagggaagg											2325
177	gtgtgggtctg	cagtccttcc	ccaggccaggg	caactgcctg	acgttgccag	atttcagctt											2385
178	cattctctctg	atagaacaaa	gcgaaatgca	gttcacacag	ggagggagac	acacaagcct											2445
179	ttttctgagg	ctcagcttcc	agacccatcc	ctgaacatgg	ggtttgaaag	gaaggtgagg											2505
180	gtgtgtggccc	ctgacagggg	acaataacac	actctactga	tgtcaccaat	ttgcaacatc											2565
181	tgccttgggt	ctagccatcc	tgggtccaaa	ttcagacct	accactcaca	agctatgtga											2625

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/925,055

DATE: 8/16/2001

TIME: 13:19:55

Input Set : A:\00-56.txt

Output Set: N:\CRF3\08162001\I925055.raw

```

195 attcaaacaa ataaatcaa tgcacagaac ctctcttctt tttcttttaa tttttttt 2685
196 ataacaacta attcatggg tctgtgtgaa tataaatca agtcatgtct ttaaatat 2745
197 taatagtggc agttacatgg agagtgcgaa ataaacata attattttaa aaaaaaaaa 2805
198 aaaaaaaaa atagcgggcg ctctga 2831
200 <210> SEQ ID NO: 2
201 <211> LENGTH: 574
202 <212> TYPE: PRT
203 <213> ORGANISM: Homo sapien
204 <400> SEQUENCE: 2
205 Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
206 1 5 10 15
207 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
208 20 25 30
209 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
210 35 40 45
211 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
212 50 55 60
213 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
214 65 70 75 80
215 Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
216 85 90 95
217 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
218 100 105 110
219 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
220 115 120 125
221 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
222 130 135 140
223 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
224 145 150 155 160
225 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
226 165 170 175
227 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
228 180 185 190
229 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
230 195 200 205
231 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
232 210 215 220
233 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
234 225 230 235 240
235 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
236 245 250 255
237 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
238 260 265 270
239 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
240 275 280 285
241 Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile
242 290 295 300
243 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Ile Gln Arg His Ser
244 305 310 315 320

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/925,055

DATE: 08-16-2001

TIME: 13:28:00

Input Set : A:\00-56.txt

Output Set : N:\CRF3\08162001\I925055.raw

```

246 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Ile Asp Ile Ser Ile Leu Gln
247           325           335
248 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
249           340           345           350
250 Pro Asn Ala Ala Pro Glu Val Gly Pro Ile Ser Tyr Ala Pro Gln Val
251           355           360           365
252 Thr Pro Glu Ala Gln Ile Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
253           370           375           380
254 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro
255           385           390           395           400
256 Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr
257           405           410           415
258 Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
259           420           425           430
260 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
261           435           440           445
262 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
263           450           455           460
264 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
265           465           470           475           480
266 Leu His Ser Gly Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
267           485           490           495
268 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
269           500           505           510
270 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
271           515           520           525
272 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
273           530           535           540
274 Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp
275           545           550           555           560
276 Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
277           565           570
281 <210> SEQ ID NO: 3
282 <211> LENGTH: 211
283 <212> TYPE: PRT
284 <213> ORGANISM: Homo sapiens
285 <400> SEQUENCE: 3
287 Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser Ser
288     1           5           10           15
289 Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro
290           20           25           30
291 Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
292           35           40           45
293 Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
294           50           55           60
295 Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
296           65           70           75           80
297 Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
298           85           90           95

```

<210> 30
 <211> 484
 <212> PRT
 <213> Artificial Sequence
 <400> 30

Extended: Field 223 is required
 When 213 response is Artificial Sequence,
 A ~~non~~ mandatory description or explanation
 is required in Field 223.

The type of errors shown ^{may} exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/925,055

DATE: 08/16/2001

TIME: 11:18:14

Input Set : A:\00-56.txt

Output Set: N:\CRF3\08162001\I925055.raw

L:11 M:270 C: Current Application Number differs, replaced Current Application No

L:11 M:271 C: Current Filing Date differs, replaced Current Filing Date

L:1093 M:258 W: Mandatory Feature missing, -21- FEATURE:

L:1093 M:258 W: Mandatory Feature missing, -21- OTHER INFORMATION: